Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 22:18:10

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6237248.sorted.bam -c -nw 400 -hm 3
```

1.2. Alignment

Command line:	/home/luna/Desktop/Software/bwa/bwa mem -t 16 -k 30 -R @RG\tID:Singlecell2022\tLB:Library\tPL:ILLUMINA\tSM:sample_SRR6237248 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6237248.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 22:18:09 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6237248.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,320,256
Mapped reads	1,783,845 / 76.88%
Unmapped reads	536,411 / 23.12%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	10,704 / 0.46%
Read min/max/mean length	30 / 76 / 76.16
Duplicated reads (estimated)	182,215 / 7.85%
Duplication rate	7.61%
Clipped reads	903,116 / 38.92%

2.2. ACGT Content

Number/percentage of A's	32,100,892 / 27.78%
Number/percentage of C's	20,456,371 / 17.7%
Number/percentage of T's	37,679,589 / 32.61%
Number/percentage of G's	25,318,320 / 21.91%
Number/percentage of N's	1,764 / 0%
GC Percentage	39.61%

2.3. Coverage

Mean	0.0373

Standard Deviation	0.501

2.4. Mapping Quality

Mean Mapping Quality	46.03

2.5. Mismatches and indels

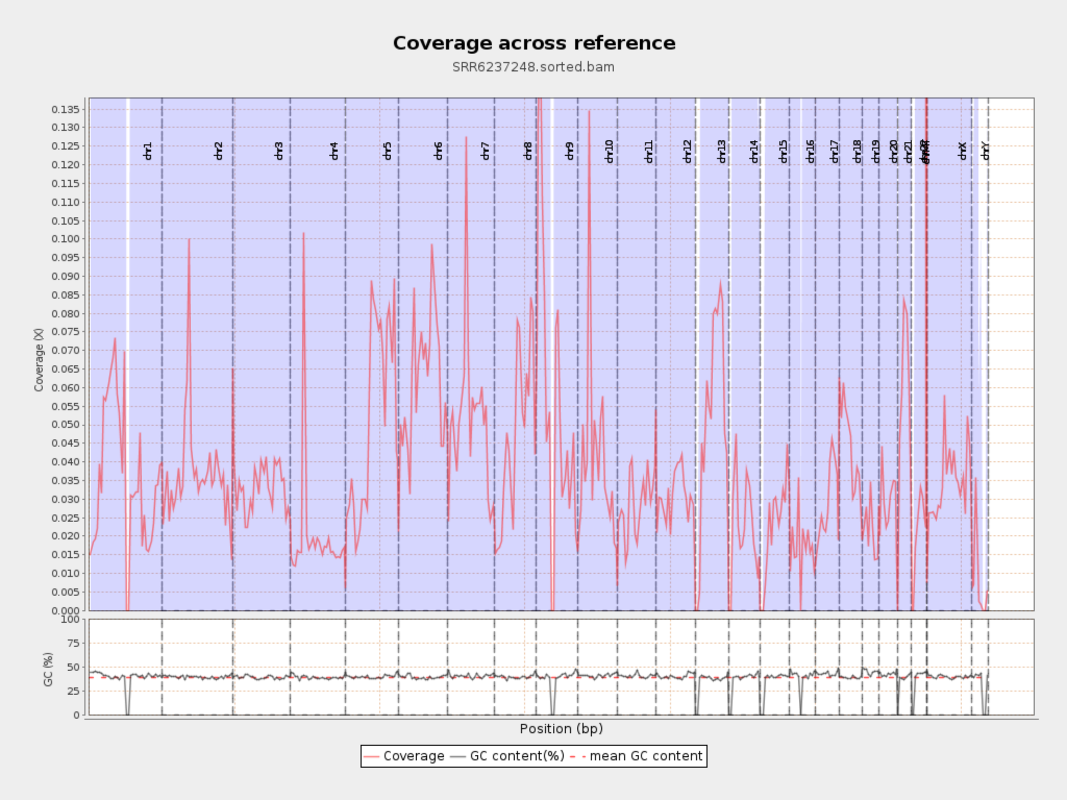
General error rate	0.89%
Mismatches	999,701
Insertions	10,423
Mapped reads with at least one insertion	0.58%
Deletions	33,351
Mapped reads with at least one deletion	1.85%
Homopolymer indels	44.66%

2.6. Chromosome stats

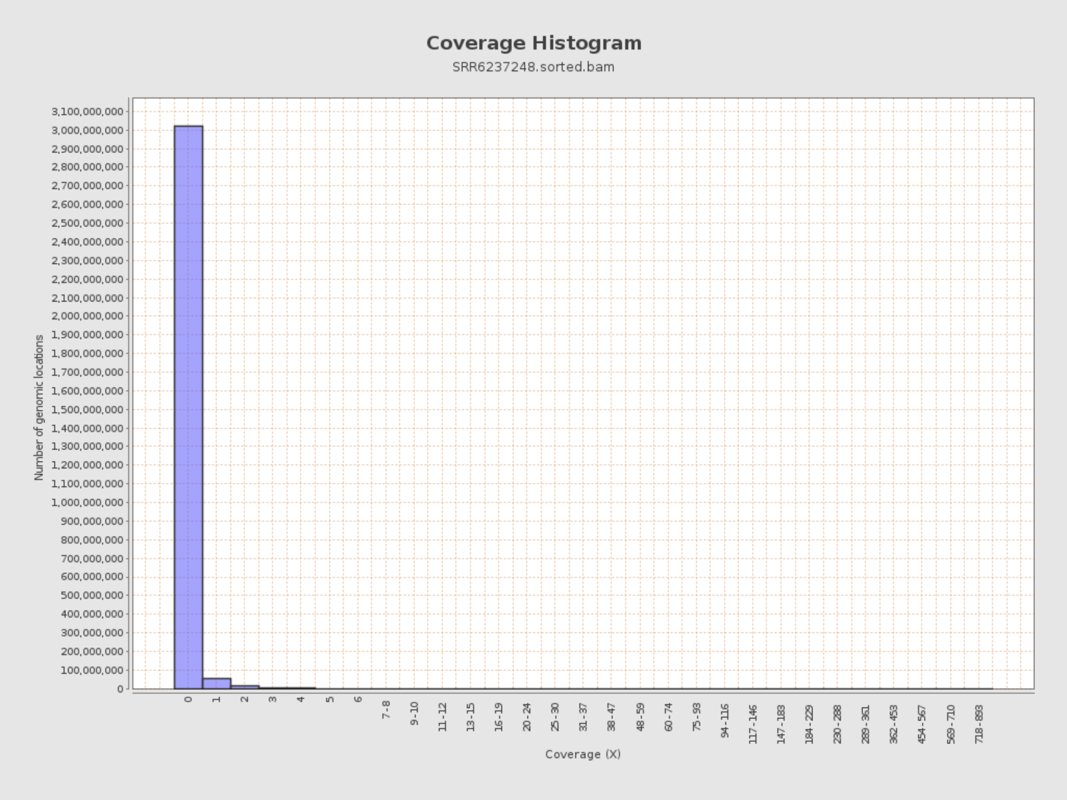
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8916562	0.0358	0.7344
chr2	243199373	9000269	0.037	0.6091
chr3	198022430	6644376	0.0336	0.2627
chr4	191154276	3780490	0.0198	0.4265
chr5	180915260	9426326	0.0521	0.3255
chr6	171115067	10514899	0.0614	0.4312
chr7	159138663	8322607	0.0523	0.8574

chr8	146364022	6776829	0.0463	0.5232
chr9	141213431	8100961	0.0574	0.5216
chr10	135534747	5588107	0.0412	0.7997
chr11	135006516	3793715	0.0281	0.3283
chr12	133851895	4077719	0.0305	0.2602
chr13	115169878	5919320	0.0514	0.3165
chr14	107349540	2303574	0.0215	0.2703
chr15	102531392	2307977	0.0225	0.2109
chr16	90354753	1534641	0.017	0.283
chr17	81195210	2343635	0.0289	0.2848
chr18	78077248	3474954	0.0445	0.8234
chr19	59128983	1302435	0.022	0.4318
chr20	63025520	1864045	0.0296	0.2802
chr21	48129895	2675266	0.0556	0.4737
chr22	51304566	1044365	0.0204	0.1975
chrMT	16571	130079	7.8498	5.3856
chrX	155270560	5337251	0.0344	0.3048
chrY	59373566	435624	0.0073	0.432

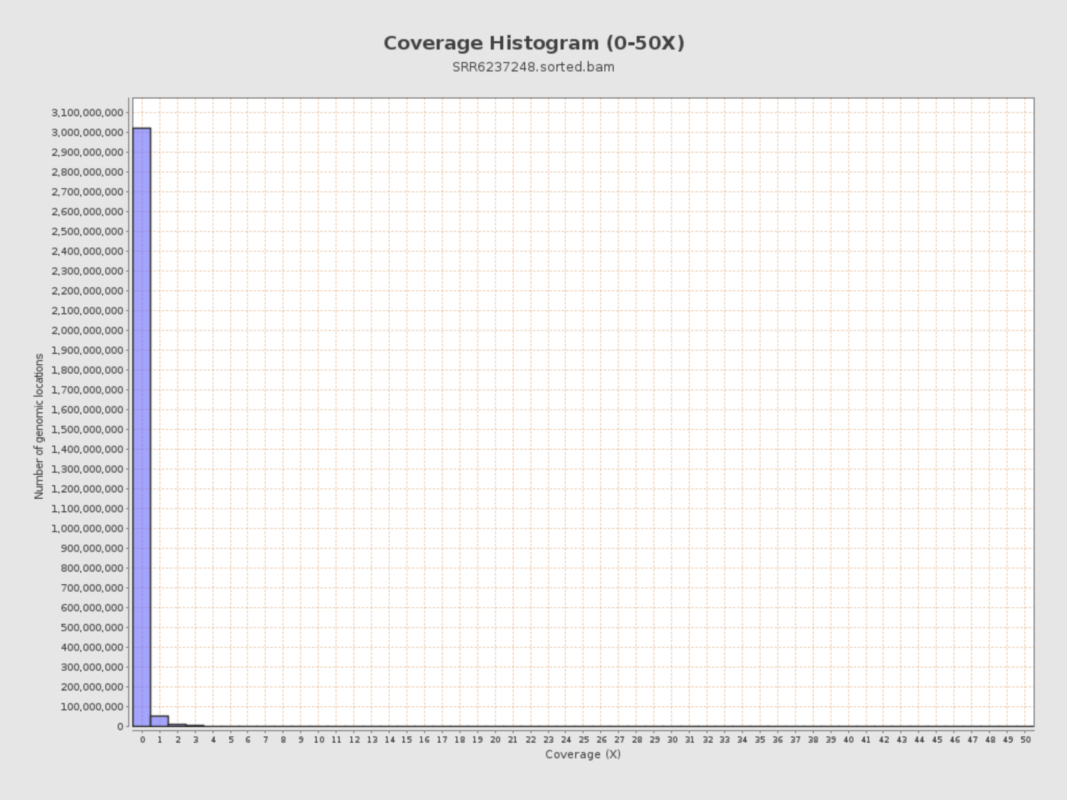
3. Results : Coverage across reference



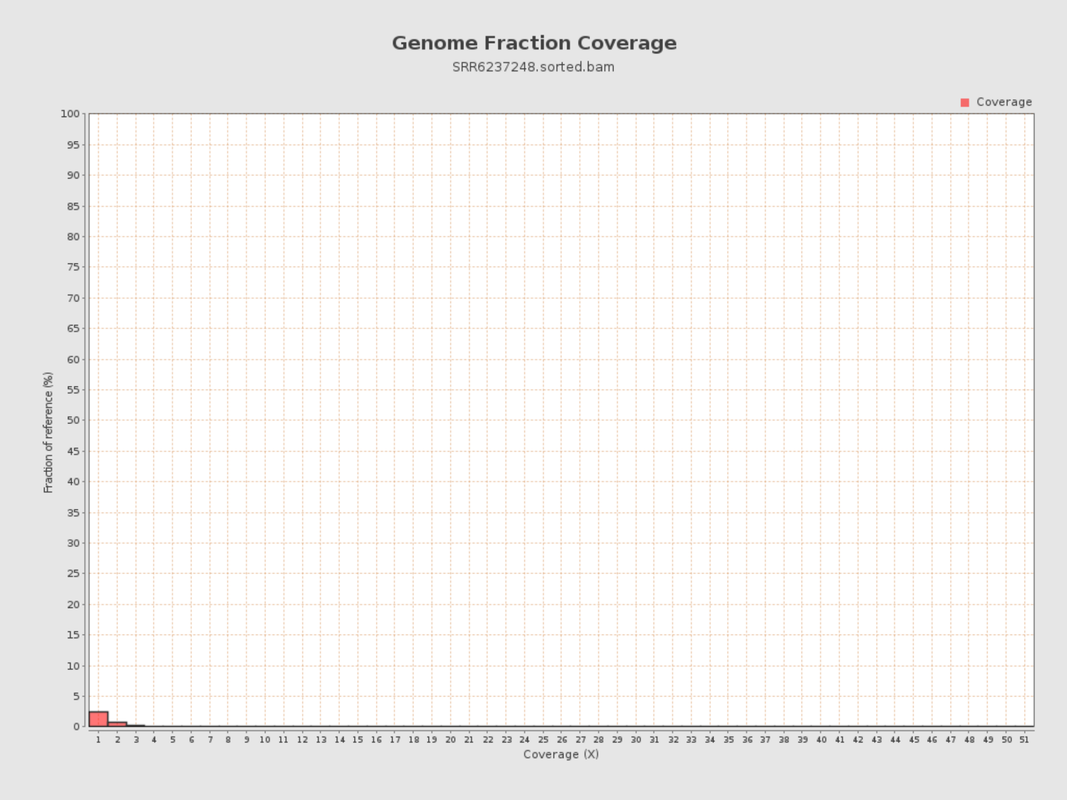
4. Results : Coverage Histogram



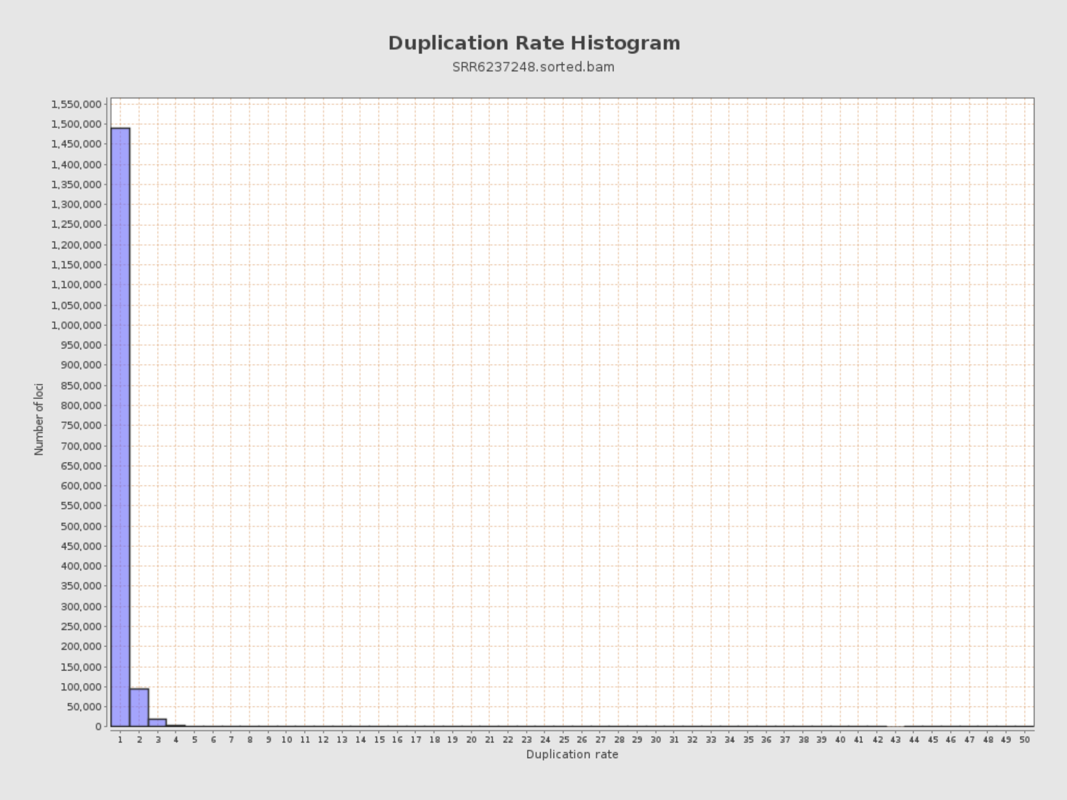
5. Results : Coverage Histogram (0-50X)



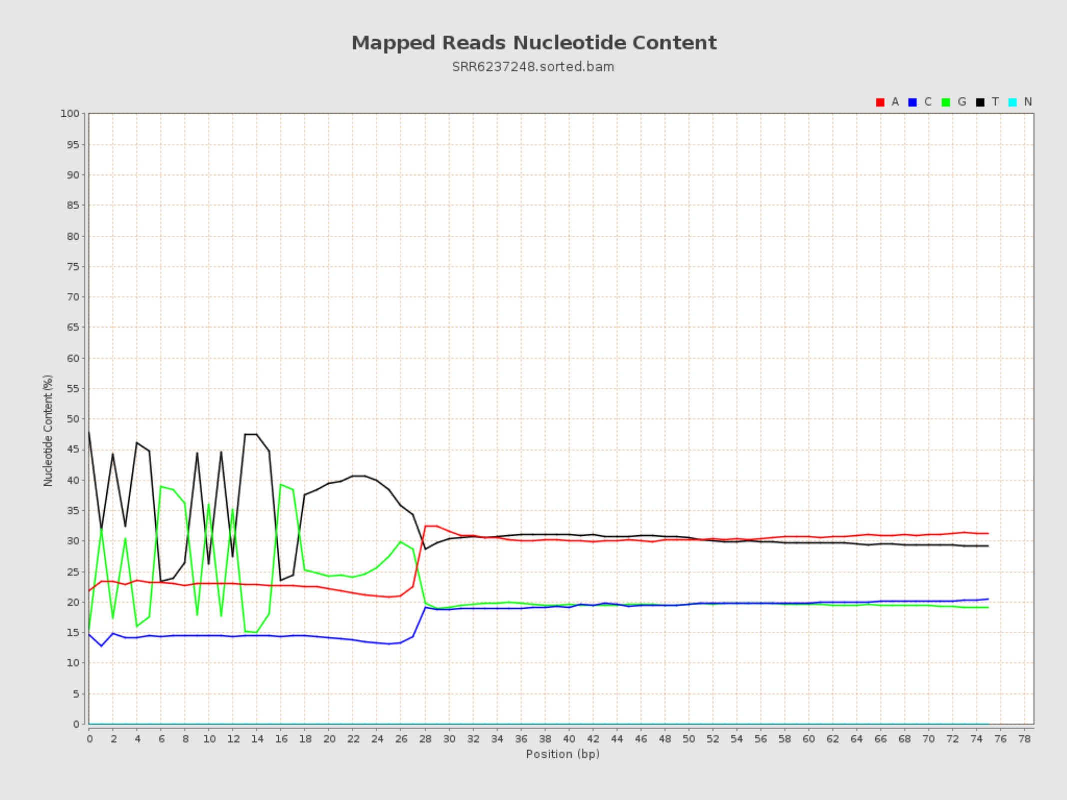
6. Results : Genome Fraction Coverage



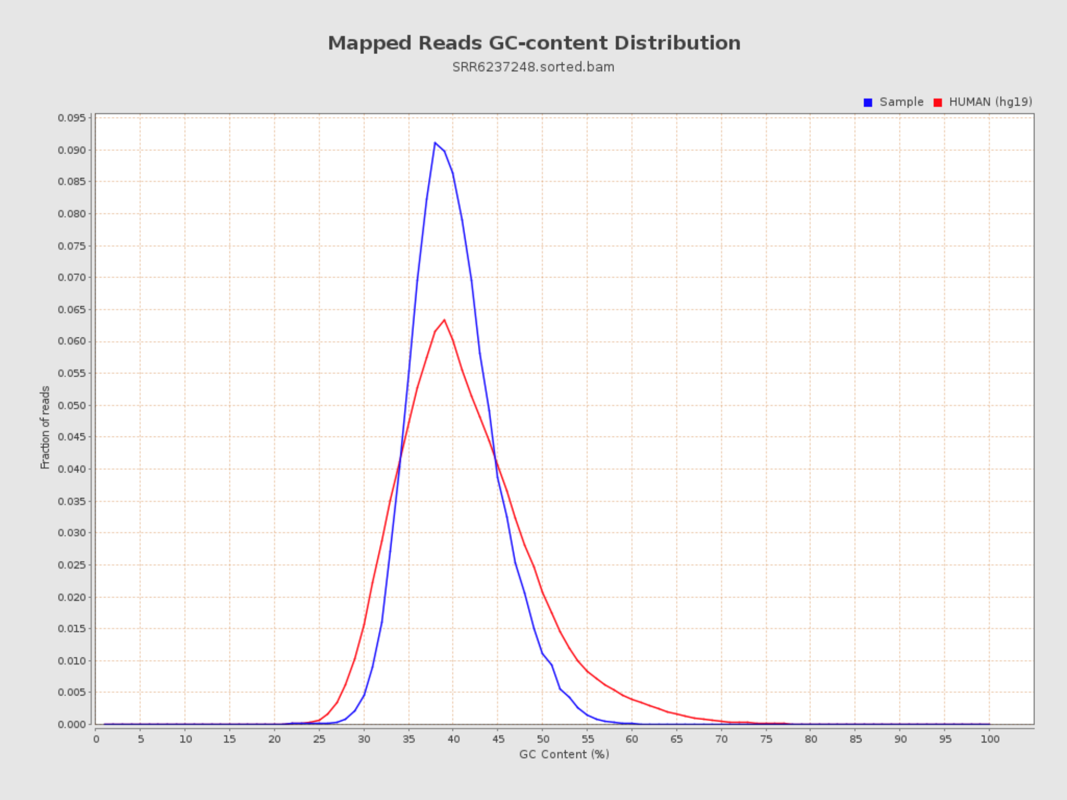
7. Results : Duplication Rate Histogram



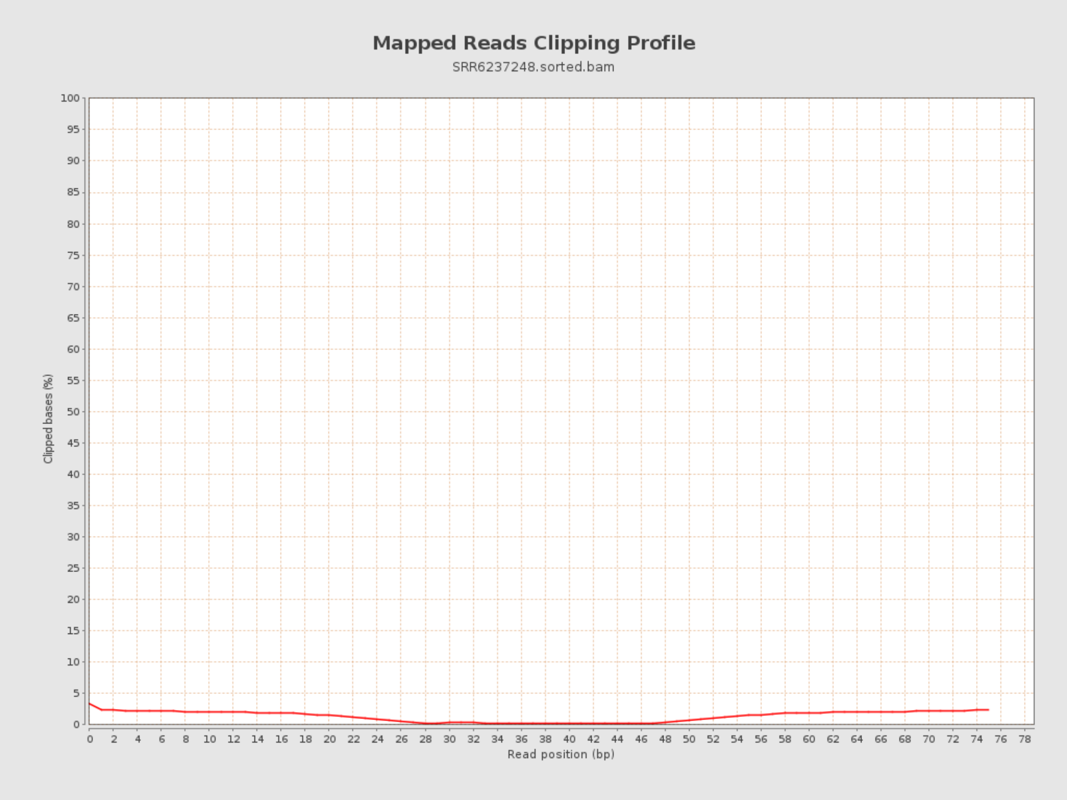
8. Results : Mapped Reads Nucleotide Content



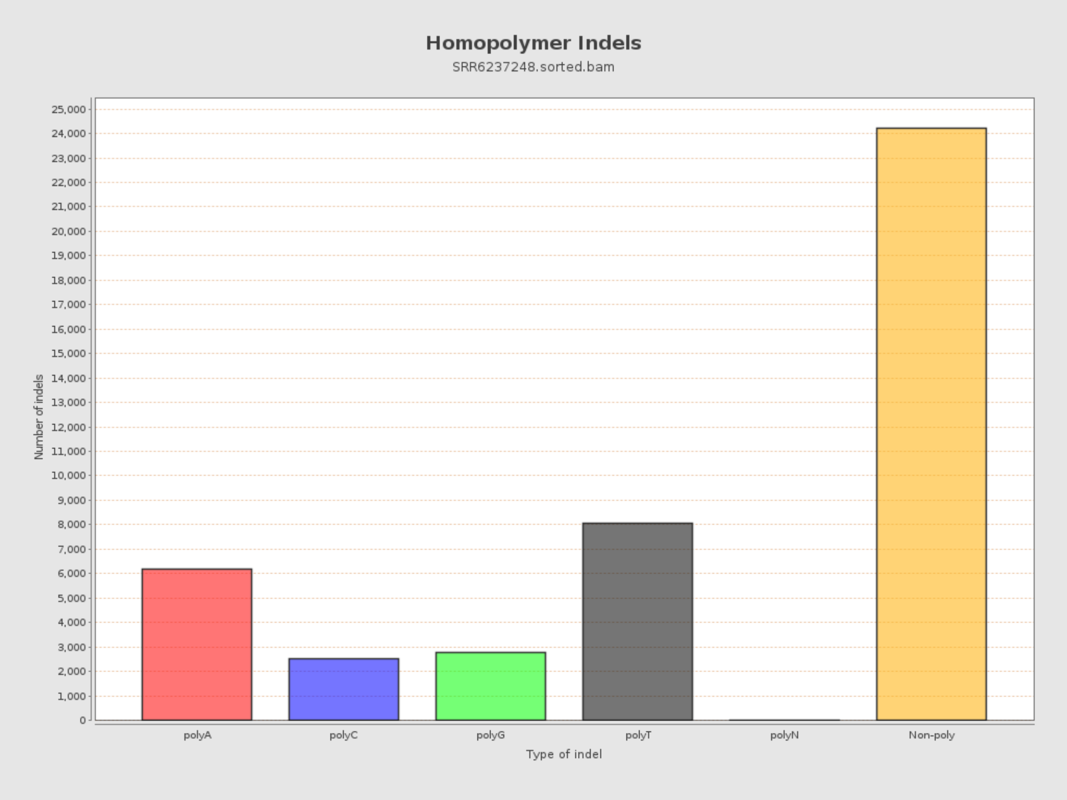
9. Results : Mapped Reads GC-content Distribution



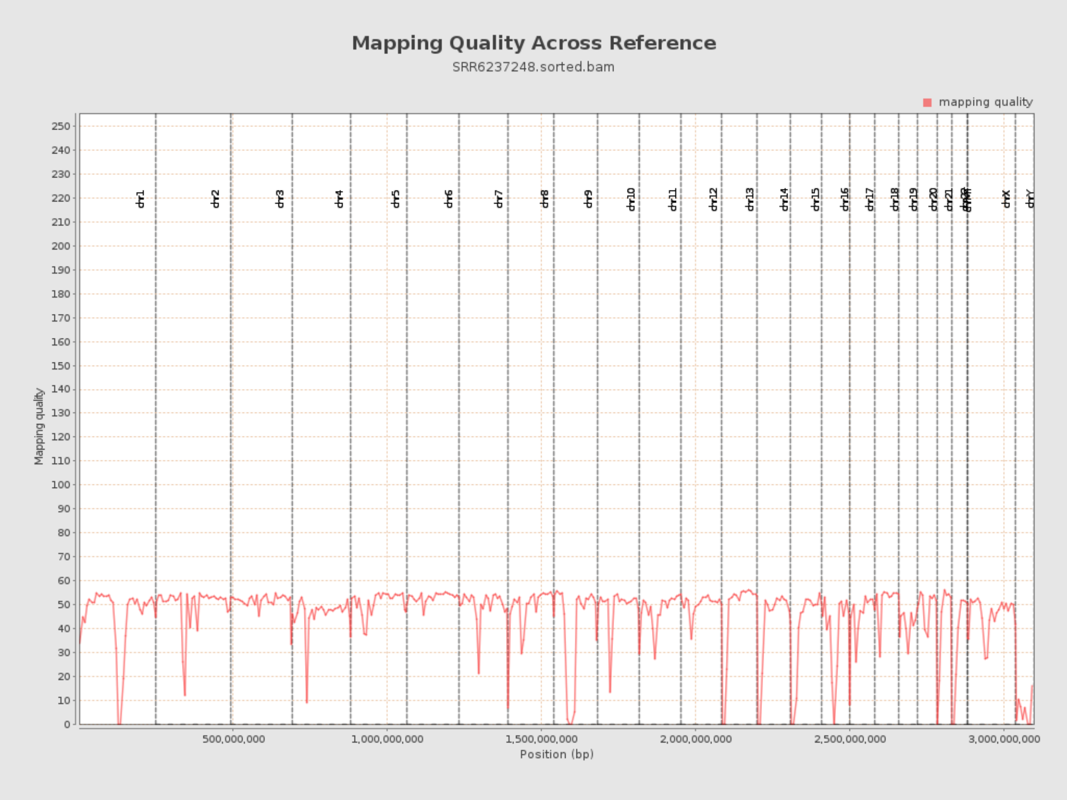
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram